

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- TY 80X
- (i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
 - (ii) TITLE OF INVENTION: Ligands for flt3 Receptors
 - (iii) NUMBER OF SEQUENCES: 8
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: March 7, 1994
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/162,407
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-D
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822
- 48

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 879 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..25

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 855..879

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGACTGGA	ACGAGACGAC	CTGCTCTGTC	ACAGGCATGA	GGGGTCCCCG	GCAGAG	56
ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG CTG	104					
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu						
1 5 10 15						
CTG TTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT TAC	152					
Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr						
20 25 30						
TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA GAG	200					
Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu						
35 40 45						
TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC AAT	248					
Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn						
50 55 60						
CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA GCC	296					
Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala						
65 70 75 80						
CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG ATG CAA	344					
Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln						
85 90 95						
ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA TGT	392					
Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys						
100 105 110						
ACC TTC CAG CCC CTA CCA GAA TGT CTG CGA TTC GTC CAG ACC AAC ATC	440					
Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile						
115 120 125						
TCC CAC CTC CTG AAG GAC ACC TGC ACA CAG CTG CTT GCT CTG AAG CCC	488					
Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro						
130 135 140						

TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG CAG 536
 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln 160
 145 150 155
 TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA GCC 584
 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala 175
 165 170
 CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG CTC 632
 Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu 190
 180 185
 CTG CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG 680
 Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp 205
 195 200
 GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT GGG 728
 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly 220
 210 215
 GTG CCC CTC CCC TCC CAT CCC TAGGATTCGA GCCTTGTGCA TCGTTGACTC 779
 Val Pro Leu Pro Ser His Pro 230
 225
 AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC AGAGCAGGAT 839
 TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC 879

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
 20 25 30
 Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
 35 40 45
 Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
 50 55 60
 Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
 65 70 75 80
 Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
 85 90 95
 Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
 100 105 110
 Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
 115 120 125

Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
 130 135 140

Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
 145 150 155 160

Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
 165 170 175

Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
 180 185 190

Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
 195 200 205

Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
 210 215 220

Val Pro Leu Pro Ser His Pro
 225 230

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGTCGT CTCGTTCCAG

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 988 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCCGGAAT TCCGGGGCCC CCGGCCGAA ATG ACA GTG CTG GCG CCA GCC TGG 53
Met Thr Val Leu Ala Pro Ala Trp
1 5

AGC CCA ACA ACC TAT CTC CTC CTG CTG CTG CTG AGC TCG GGA CTC 101
Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Ser Ser Gly Leu
10 15 20

AGT GGG ACC CAG GAC TGC TCC TTC CAA CAC AGC CCC ATC TCC TCC GAC 149
Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
25 30 35 40

TTC GCT GTC AAA ATC CGT GAG CTG TCT GAC TAC CTG CTT CAA GAT TAC 197
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
45 50 55

CCA GTC ACC GTG GCC TCC AAC CTG CAG GAC GAG GAG CTC TGC GGG GGC 245
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly
60 65 70

CTC TGG CGG CTG GTC CTG GCA CAG CGC TGG ATG GAG CGG CTC AAG ACT 293
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
75 80 85

GTC GCT GGG TCC AAG ATG CAA GGC TTG CTG GAG CGC GTG AAC ACG GAG 341
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu
90 95 100

ATA CAC TTT GTC ACC AAA TGT GCC TTT CAG CCC CCC CCC AGC TGT CTT 389
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu
105 110 115 120

CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC GAG 437
Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu
125 130 135

CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC CGG 485
Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg
140 145 150

TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC CCA 533
Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro
155 160 165

5 TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC 581
Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro
170 175 180

CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC 629
Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala
185 190 195 200

GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC 677
Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg
205 210 215

CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT 725
 Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu
 220 225 230

GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTAAACAAC 774
 Val Glu His
 235

GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG CACACAGAGG 834

GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC 894

CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC 954

GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG 988

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu	1	5	10	15
Leu	Leu	Leu	Leu	Ser	Ser	Gly	Leu	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	20	25	30	
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	35	40	45	
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	50	55	60	
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	65	70	75	80
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	85	90	95	
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	100	105	110	
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	115	120	125	
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	130	135	140	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	145	150	155	160
Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Ala	165	170	175	
Thr	Ala	Pro	Thr	Ala	Pro	Gln	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	180	185	190	
Pro	Val	Gly	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Trp	Cys	Leu	His	Trp	Gln	195	200	205	

Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val
210 215 220

Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His
225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 60

ACTTCAGCCA C 71

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG 37

08993966-121897

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